

Dietmar Spengler and Laurent Journot
Serial No.: 09/254,870
Filed: August 16, 1999
Page 2

comply with the Sequence Rules and that applicants must provide
1) a substitute computer readable form (CRF) copy of the
"Sequence Listing"; 2) a substitute paper copy of the "Sequence
Listing ", as well as an amendment directing its entry into the
specification; AND 3) a statement that the content of the paper
and computer readable copies are the same and, where applicable,
include no new matter, as required by 37 C.F.R. §1.821(e) or
§1.821(f) or §1.821(g) or §1.825(b) or §1.825(d).

Please amend the specification as follows:

In the Specification

Please delete the previously submitted paper copy of the
"Sequence Listing" inserted after page 71.

Please insert after page 71 the amended paper copy of the
"Sequence Listing", attached to hereto as **Exhibit B**.

REMARKS

In response to the August 17, 2000 Notice, applicants submit
herewith a computer readable form (CRF) copy of a revised
Sequence Listing which is set forth on the newly submitted paper
copy of revised Sequence Listing.

Applicants further submit a paper copy of the revised Sequence
Listing, attached hereto as **Exhibit B**, and a Statement in
Accordance with 37 C.F.R. §1.821(f), attached hereto as **Exhibit
C**, certifying that the computer readable form as required by 37
C.F.R. §1.821(e) is identical to the paper copy of Sequence

C

Dietmar Spengler and Laurent Journot
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Page 3

32 2000

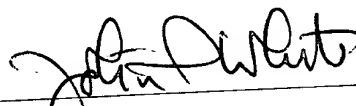
TECH CENTER 1600/2900

Listing.

Applicants are submitting herewith a computer diskette containing
a C.F.R. of the sequence listing.

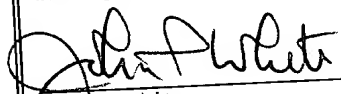
No fee is deemed necessary in connection with the filing of this
Amendment. However, if any fee is required, authorization is
hereby given to charge the amount of any such fee to Deposit
Account No. 03-3125.

Respectfully submitted,



John P. White
Registration No. 28,678
Attorney for Applicants
Cooper & Dunham LLP
1185 Avenue of the Americas
New York, New York 10036
(212) 278-0400

I hereby certify that this correspondence
is being deposited this date with the U.S.
Postal Service with sufficient postage as
first class mail addressed to: Assistant
Commissioner for Patents and Trademarks,
Washington, D.C. 20231.

 9/18/02
Date
John P. White
Reg. No. 28,678

UNITED STATES DEPARTMENT OF COMMERCE
Patent Trademark Office
COMMISSIONER OF PATENTS AND
TRADEMARKS
Washington, D.C. 20231

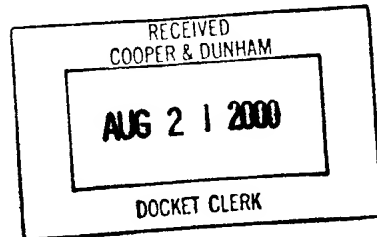
JPW



DEA/FCE-1994

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.

8/17/00
9/17/00
10/17/00
11/17/00
11/24/00 (NON-EXT)
W.D.



EXAMINER	
ART UNIT	PAPER NUMBER
	10

received
MAILED: 8/23/00

Please find below a communication from the EXAMINER in charge of this application
Commissioner of Patents

The reply filed on 6/29/00 is not fully responsive to the communication mailed on 5/24/00 for the reasons set forth on the attached Raw Sequence Listing Error Report.

Since the above-mentioned reply appears to be bona fide, applicant is given a TIME PERIOD of ONE (1) MONTH or THIRTY (30) DAYS, from the mailing date of this notice, whichever is longer, within which to supply the omission or correction in order to avoid abandonment. EXTENSIONS OF THIS TIME PERIOD MAY BE GRANTED UNDER 37 CFR 1.136(a).

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Charles L. Patterson, Jr., Ph.D. whose telephone number is (703) 308-1834. The examiner can normally be reached on any day of the week from 7:30 AM until 4:00 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ponnathapu Achutamurthy, can be reached on (703) 308-3804. The fax phone number for this Group is (703) 305-7401.

Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Patterson
August 15, 2000

CHARLES L. PATTERSON, JR.
PRIMARY EXAMINER
GROUP 1800

C



RECEIVED

SEP 28 2001

Dkt. 52130-A-PCT-US/JPW/EP
TECH CENTER

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants : Dietmar Spengler and Laurent Journot
Serial No. : 09/254,870 Examiner: C. Patterson
Filed : August 16, 1999 Group Art Unit: 1652
For : NUCLEIC ACID MOLECULES CODING FOR TUMOR
SUPPRESSOR PROTEINS AND METHODS FOR THEIR
ISOLATION

1185 Avenue of the Americas
New York, New York 10036
September 18, 2000

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

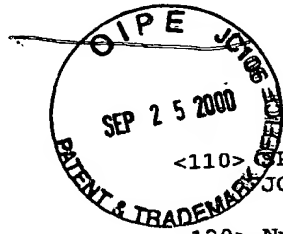
STATEMENT IN ACCORDANCE WITH 37 C.F.R. §1.821(f)

In accordance with 37 C.F.R. §1.821(f), I hereby certify that the enclosed computer readable form containing the nucleic acid and/or amino acid sequences required by 37 C.F.R. §1.821(f) has the same information which is submitted as the paper copy of the "Sequence Listing" attached hereto as **Exhibit B**.

Respectfully submitted,

Elizabeth M. Wieckowski
Elizabeth M. Wieckowski
Registration No. 42,226
Cooper & Dunham LLP
1185 Avenue of the Americas
New York, New York 10036
(212) 278-0400

C



Attachment
C1

SEQUENCE LISTING

<110> SPENGLER, Dietmar
JOURNOT, Laurent

<120> Nucleic acid molecules coding for tumor suppressor
proteins and methods for their isolation

<130> 52130-A-PCT-US

<140> 09/254,870
<141> 1997-09-22

<160> 17

<170> PatentIn Ver. 2.1

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<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (542)..(2542)

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tcagcgtgcc atcggtctcg tatttgcata ggagtcagag gagttaatct tgtctcctcg 240
aagatagact ctcatggttt atgateccatc tctgtgagaa gactttattt gtctgtctct 300
tctcacaggt ttgagtcttc agacttctac agaactccat aatatctgcc tcacagctgg 360
ctttctctgt ctcacagaag acaccagct attgtgctct ggatctctcc tggctgctag 420
gctgtagcgc tgcctttctg ggtcaggct gtagtgactc cccaccttct ttctgtctgg 480
gcttaaatgg cacagcagtt cctcagcaca tctgaagaag aaagtgtgag aaccaaaggg 540
c atg gct cca ttc cgc tgt caa aaa tgt ggc aag tcc ttc gtc acc ctg 589
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1 5 10 15
gag aag ttc acc att cac aat tat tcc cac tcc agg gag cgc cca ttc 637
Glu Lys Phe Thr Ile His Asn Tyr Ser His Ser Arg Glu Arg Pro Phe
20 25 30
aag tgc tgc aag gct gag tgt ggc aaa gcc ttc gtc tcc aag tat aag 685
Lys Cys Ser Lys Ala Glu Cys Gly Lys Ala Phe Val Ser Lys Tyr Lys
35 40 45
ctg atg aga cac atg gcc aca cac tgc cca cag aag att cac cag tgt 733
Leu Met Arg His Met Ala Thr His Ser Pro Gln Lys Ile His Gln Cys
50 55 60
act cac tgt gag aag aca ttc aac cgg aag gac cac ctg aag aac cac 781
Thr His Cys Glu Lys Thr Phe Asn Arg Lys Asp His Leu Lys Asn His

75

C

65	70	75	80	
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Leu Gln Thr His Asp Pro Asn Lys Ile Ser Tyr Ala Cys Asp Cys				
	85	90	95	
ggc aag aag tac cac acc atg ctg ggc tac aag agg cac ctg gcc ctg				877
Gly Lys Lys Tyr His Thr Met Leu Gly Tyr Lys Arg His Leu Ala Leu				
	100	105	110	
cac tcg gcg agc aat ggc gat ctc acc tgt ggg gtg tgc acc ctg gag				925
His Ser Ala Ser Asn Gly Asp Leu Thr Cys Gly Val Cys Thr Leu Glu				
	115	120	125	
ctg ggg agc acc gag gtc ctg ctg gac cac ctc aag tct cac gcg gaa				973
Leu Gly Ser Thr Glu Val Leu Leu Asp His Leu Lys Ser His Ala Glu				
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gaa aag gcc aac cag gca ccc agg gag aag aaa tac cag tgc gac cac				1021
Glu Lys Ala Asn Gln Ala Pro Arg Glu Lys Lys Tyr Gln Cys Asp His				
	145	150	155	160
tgt gat aga tgc ttc tac acc cgg aaa gat gtg cgt cgc cac ctg gtg				1069
Cys Asp Arg Cys Phe Tyr Thr Arg Lys Asp Val Arg Arg His Leu Val				
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gtc cac aca gga tgc aag gac ttc ctg tgt cag ttc tgt gcc cag aga				1117
Val His Thr Gly Cys Lys Asp Phe Leu Cys Gln Phe Cys Ala Gln Arg				
	180	185	190	
ttt ggg cgc aaa gac cac ctc act cgt cac acc aag aag acc cac tcc				1165
Phe Gly Arg Lys Asp His Leu Thr Arg His Thr Lys Lys Thr His Ser				
	195	200	205	
cag gag ctg atg caa gag aat atg cag gca gga gat tac cag agc aat				1213
Gln Glu Leu Met Gln Glu Asn Met Gln Ala Gly Asp Tyr Gln Ser Asn				
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Phe Gln Leu Ile Ala Pro Ser Thr Ser Phe Gln Ile Lys Val Asp Pro				
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Met Pro Pro Phe Gln Leu Gly Ala Ala Pro Glu Asn Gly Leu Asp Gly				
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ggc ttg cca ccc gag gtt cat ggt cta gtg ctt gct gcc cca gaa gaa				1357
Gly Leu Pro Pro Glu Val His Gly Leu Val Leu Ala Ala Pro Glu Glu				
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gct ccc caa ccc atg ccg ccc ttg gag cct ttg gag cct ttg gag cct				1405
Ala Pro Gln Pro Met Pro Pro Leu Glu Pro Leu Glu Pro Leu Glu Pro				
	275	280	285	
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Leu Glu Pro Leu Glu Pro Met Gln Ser Leu Glu Pro Leu Gln Pro Leu				
	290	295	300	
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Glu Pro Met Gln Pro Leu Glu Pro Met Gln Pro Leu Glu Pro Met Gln				
	305	310	315	320
cct tta gag cct ttg gag cct ctg gag ccg atg cag cct ttg gag ccg				1549

Pro Leu Glu Pro Leu Glu Pro Leu Glu Pro Met Gln Pro Leu Glu Pro
 325 330 335

atg cag cct ttg gag cct atg cag cca atg ctg cca atg cag cca atg 1597
 Met Gln Pro Leu Glu Pro Met Gln Pro Met Leu Pro Met Gln Pro Met
 340 345 350

cag cca atg cag cca atg cag cca atg ctg cca atg cag cca atg ctg 1645
 Gln Pro Met Gln Pro Met Gln Pro Met Leu Pro Met Gln Pro Met Leu
 355 360 365

cca atg cag cca atg cag cca atg cag cca atg ctg cca atg cca gag 1693
 Pro Met Gln Pro Met Gln Pro Met Gln Pro Met Leu Pro Met Pro Glu
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ccg tct ttc act ctg cac cct ggc gta gtt ccc acc tct cct ccc cca 1741
 Pro Ser Phe Thr Leu His Pro Gly Val Val Pro Thr Ser Pro Pro Pro
 385 390 395 400

att att ctt cag gag cat aag tat aat cct gtt cct acc tca tat gcc 1789
 Ile Ile Leu Gln Glu His Lys Tyr Asn Pro Val Pro Thr Ser Tyr Ala
 405 410 415

cca ttt gta ggc atg ccc gtc aaa gca gat ggc aag gcc ttt tgc aac 1837
 Pro Phe Val Gly Met Pro Val Lys Ala Asp Gly Lys Ala Phe Cys Asn
 420 425 430

gtg ggt ttc ttt gag gaa ttt cct ctg caa gag cct cag gcg cct ctc 1885
 Val Gly Phe Phe Glu Glu Phe Pro Leu Gln Glu Pro Gln Ala Pro Leu
 435 440 445

aag ttc aac cca tgt ttt gag atg cct atg gag ggg ttt ggg aaa gtc 1933
 Lys Phe Asn Pro Cys Phe Glu Met Pro Met Glu Gly Phe Gly Lys Val
 450 455 460

acc ctg tcc aaa gag ctg ctg gta gat gct gtg aat ata gcc att cct 1981
 Thr Leu Ser Lys Glu Leu Leu Val Asp Ala Val Asn Ile Ala Ile Pro
 465 470 475 480

gcc tct ctg gag att tcc tcc cta ttg ggg ttt tgg cag ctc ccc cct 2029
 Ala Ser Leu Glu Ile Ser Ser Leu Leu Gly Phe Trp Gln Leu Pro Pro
 485 490 495

cct act ccc cag aat ggc ttt gtg aat agc acc atc cct gtg ggg cct 2077
 Pro Thr Pro Gln Asn Gly Phe Val Asn Ser Thr Ile Pro Val Gly Pro
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ggg gag cca ctg ccc cat agg ata acc tgt ctg gcg cag cag cag cca 2125
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 515 520 525

ccg cca ctg ccg ccg cca cca ccg ctg cca ctg cca cag cca ctg cca 2173
 Pro Pro Leu Pro Pro Pro Pro Pro Leu Pro Leu Pro Gln Pro Leu Pro
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gtg cca cag cca cta cca cag cca cag atg cag cca cag ttt cag ttg 2221
 Val Pro Gln Pro Leu Pro Gln Pro Gln Met Gln Pro Gln Phe Gln Leu
 545 550 555 560

cag atc cag ccc cag atg cag cta cca cag ctg ctg ccg caa ctg caa 2269
 Gln Ile Gln Pro Gln Met Gln Leu Pro Gln Leu Leu Pro Gln Leu Gln
 565 570 575

cct cag cag cag cct gat cct gag cca gag cca gag cca gag cca gag 2317
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 580 585 590

cca gag cca gag cca gag ccg gaa ccg gaa ccg gag cca gag cca gag 2365
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 Pro Glu Pro Glu Pro Glu Glu Glu Gln Glu Glu Ala Glu Glu Glu Ala
 610 615 620

gag gaa gga gca gag gaa gga gca gaa cca gag gca cag gca gaa gaa 2461
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 625 630 635 640

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 Ile Ala Gly Leu Val Tyr Lys Lys Trp Thr Val
 660 665

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 65 70 75 80

Leu Gln Thr His Asp Pro Asn Lys Ile Ser Tyr Ala Cys Asp Asp Cys
 85 90 95

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 100 105 110

His Ser Ala Ser Asn Gly Asp Leu Thr Cys Gly Val Cys Thr Leu Glu
 115 120 125

Leu Gly Ser Thr Glu Val Leu Leu Asp His Leu Lys Ser His Ala Glu
 130 135 140
 Glu Lys Ala Asn Gln Ala Pro Arg Glu Lys Lys Tyr Gln Cys Asp His
 145 150 155 160
 Cys Asp Arg Cys Phe Tyr Thr Arg Lys Asp Val Arg Arg His Leu Val
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 Val His Thr Gly Cys Lys Asp Phe Leu Cys Gln Phe Cys Ala Gln Arg
 180 185 190
 Phe Gly Arg Lys Asp His Leu Thr Arg His Thr Lys Lys Thr His Ser
 195 200 205
 Gln Glu Leu Met Gln Glu Asn Met Gln Ala Gly Asp Tyr Gln Ser Asn
 210 215 220
 Phe Gln Leu Ile Ala Pro Ser Thr Ser Phe Gln Ile Lys Val Asp Pro
 225 230 235 240
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 Ala Pro Gln Pro Met Pro Pro Leu Glu Pro Leu Glu Pro Leu Glu Pro
 275 280 285
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 290 295 300
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 305 310 315 320
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 325 330 335
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Thr Leu Ser Lys Glu Leu Leu Val Asp Ala Val Asn Ile Ala Ile Pro
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 Ala Ser Leu Glu Ile Ser Ser Leu Leu Gly Phe Trp Gln Leu Pro Pro
 485 490 495
 Pro Thr Pro Gln Asn Gly Phe Val Asn Ser Thr Ile Pro Val Gly Pro
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 Gly Glu Pro Leu Pro His Arg Ile Thr Cys Leu Ala Gln Gln Gln Pro
 515 520 525
 Pro Pro Leu Pro Pro Pro Pro Pro Leu Pro Leu Pro Gln Pro Leu Pro
 530 535 540
 Val Pro Gln Pro Leu Pro Gln Pro Gln Met Gln Pro Gln Phe Gln Leu
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 610 615 620
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 <213> Artificial Sequence

<220>
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36

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<400> 4

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 <213> Mus sp.

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 <211> 9
 <212> PRT
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 primer

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 or T

<220>
 <223> Xaa at position 7 is a cross-link representing F
 or Y

<220>
 <223> Xaa at position 8 can be any amino acid

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81

C

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<210> 10
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<220>
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 primer

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<220>
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33

82

C

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<220>
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<210> 15
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<220>
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 primer

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<220>
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 <222> (803)..(2191)

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 aatatattat gtaagcaatt ttgtgtgttc ttttttttcc acttgcataa agcaggggaa 180
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Met	Ala	Thr	Phe	Pro	Cys	Gln	Leu	Cys	Gly							
1				5					10							
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Lys	Thr	Phe	Leu	Thr	Leu	Glu	Lys	Phe	Thr	Ile	His	Asn	Tyr	Ser	His	
			15					20						25		
tcc	agg	gag	cgg	ccg	tac	aag	tgt	gtg	cag	cct	gac	tgt	ggc	aaa	gcc	928
Ser	Arg	Glu	Arg	Pro	Tyr	Lys	Cys	Val	Gln	Pro	Asp	Cys	Gly	Lys	Ala	
		30						35					40			
ttt	gtt	tcc	aga	tat	aaa	ttg	atg	agg	cat	atg	gct	acc	cat	tct	ccc	976
Phe	Val	Ser	Arg	Tyr	Lys	Leu	Met	Arg	His	Met	Ala	Thr	His	Ser	Pro	
		45					50					55				
cag	aaa	tct	cac	cag	tgt	gct	cac	tgt	gag	aag	acg	ttc	aac	cgg	aaa	1024
Gln	Lys	Ser	His	Gln	Cys	Ala	His	Cys	Glu	Lys	Thr	Phe	Asn	Arg	Lys	
	60					65					70					
gac	cac	ctg	aaa	aac	cac	ctc	cag	acc	cac	gac	ccc	aac	aaa	atg	gcc	1072
Asp	His	Leu	Lys	Asn	His	Leu	Gln	Thr	His	Asp	Pro	Asn	Lys	Met	Ala	
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Phe	Gly	Cys	Glu	Glu	Cys	Gly	Lys	Lys	Tyr	Asn	Thr	Met	Leu	Gly	Tyr	
			95						100					105		
aag	agg	cac	ctg	gcc	ctc	cat	gcg	gcc	agc	agt	ggg	gac	ctc	acc	tgt	1168
Lys	Arg	His	Leu	Ala	Leu	His	Ala	Ala	Ser	Ser	Gly	Asp	Leu	Thr	Cys	
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ggg	gtc	tgt	gcc	ctg	gag	cta	ggg	agc	acc	gag	gtg	cta	ctg	gac	cac	1216
Gly	Val	Cys	Ala	Leu	Glu	Leu	Gly	Ser	Thr	Glu	Val	Leu	Leu	Asp	His	
		125					130					135				
ctc	aaa	gcc	cat	gcg	gaa	gag	aag	ccc	cct	agc	gga	acc	aag	gaa	aag	1264
Leu	Lys	Ala	His	Ala	Glu	Glu	Lys	Pro	Pro	Ser	Gly	Thr	Lys	Glu	Lys	
	140					145					150					
aag	cac	cag	tgc	gac	cac	tgt	gaa	aga	tgc	ttc	tac	acc	cgg	aag	gat	1312
Lys	His	Gln	Cys	Asp	His	Cys	Glu	Arg	Cys	Phe	Tyr	Thr	Arg	Lys	Asp	
	155				160					165					170	
gtg	cga	cgc	cac	ctg	gtg	gtc	cac	aca	gga	tgc	aag	gac	ttc	ctg	tgc	1360
Val	Arg	Arg	His	Leu	Val	Val	His	Thr	Gly	Cys	Lys	Asp	Phe	Leu	Cys	
			175						180					185		
cag	ttc	tgt	gcc	cag	aga	ttt	ggg	cgc	aag	gat	cac	ctc	acc	cgg	cat	1408
Gln	Phe	Cys	Ala	Gln	Arg	Phe	Gly	Arg	Lys	Asp	His	Leu	Thr	Arg	His	
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acc	aag	aag	acc	cac	tca	cag	gag	ctg	atg	aaa	gag	agc	ttg	cag	acc	1456
Thr	Lys	Lys	Thr	His	Ser	Gln	Glu	Leu	Met	Lys	Glu	Ser	Leu	Gln	Thr	
		205					210					215				
gga	gac	ctt	ctg	agc	acc	ttc	cac	acc	atc	tcg	cct	tca	ttc	caa	ctg	1504
Gly	Asp	Leu	Leu	Ser	Thr	Phe	His	Thr	Ile	Ser	Pro	Ser	Phe	Gln	Leu	
	220					225					230					
aag	gct	gct	gcc	ttg	cct	cct	ttc	cct	tta	gga	gct	tct	gcc	cag	aac	1552
Lys	Ala	Ala	Ala	Leu	Pro	Pro	Phe	Pro	Leu	Gly	Ala	Ser	Ala	Gln	Asn	
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 Gly Leu Ala Ser Ser Leu Pro Ala Glu Val His Ser Leu Thr Leu Ser
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ccc cca gaa caa gcc gcc cag cct atg cag ccg ctg cca gag tcc ctg 1648
 Pro Pro Glu Gln Ala Ala Gln Pro Met Gln Pro Leu Pro Glu Ser Leu
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gcc tcc ctc cac ccc tgg gta tcc cct ggc tct cct ccg cca ccc ctt 1696
 Ala Ser Leu His Pro Ser Val Ser Pro Gly Ser Pro Pro Pro Leu
 285 290 295

ccc aat cac aag tac aac acc act tct acc tca tac tcc cca ctt gca 1744
 Pro Asn His Lys Tyr Asn Thr Thr Ser Thr Ser Tyr Ser Pro Leu Ala
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agc ctg ccc ctc aaa gca gat act aaa ggt ttt tgc aat atc agt ttg 1792
 Ser Leu Pro Leu Lys Ala Asp Thr Lys Gly Phe Cys Asn Ile Ser Leu
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 Phe Glu Asp Leu Pro Leu Gln Glu Pro Gln Ser Pro Gln Lys Leu Asn
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cca ggt ttt gat ctg gct aag gga aat gct ggt aaa gta aac ctg ccc 1888
 Pro Gly Phe Asp Leu Ala Lys Gly Asn Ala Gly Lys Val Asn Leu Pro
 350 355 360

aag gag ctg cct gca gat gct gtg aac cta aca ata cct gcc tct ctg 1936
 Lys Glu Leu Pro Ala Asp Ala Val Asn Leu Thr Ile Pro Ala Ser Leu
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gac ctg tcc ccc ctg ttg ggc ttc tgg cag ctg ccc cct cct gct acc 1984
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caa aat acc ttt ggg aat agc act ctt gcc ctg ggg cct ggg gaa tct 2032
 Gln Asn Thr Phe Gly Asn Ser Thr Leu Ala Leu Gly Pro Gly Glu Ser
 395 400 405 410

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 Leu Pro His Arg Leu Ser Cys Leu Gly Gln Gln Gln Gln Glu Pro Pro
 415 420 425

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 Leu Ala Met Gly Thr Val Ser Leu Gly Gln Leu Pro Leu Pro Pro Ile
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cct cat gtg ttc tca gct ggc act ggc tct gcc atc ctg cct cat ttc 2176
 Pro His Val Phe Ser Ala Gly Thr Gly Ser Ala Ile Leu Pro His Phe
 445 450 455

cat cat gca ttc aga taattgattt ttaaagtgtat tttttcgtat tctggaagat 2231
 His His Ala Phe Arg
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gttttaagaa gcattttaaa tgtcagttac aatatgagaa agatttgga aacgagactg 2291

ggactatggc ttattcagtg atgactggct tgagatgata aga 2334

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Lys Cys Val Gln Pro Asp Cys Gly Lys Ala Phe Val Ser Arg Tyr Lys
 35 40 45

Leu Met Arg His Met Ala Thr His Ser Pro Gln Lys Ser His Gln Cys
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Ala His Cys Glu Lys Thr Phe Asn Arg Lys Asp His Leu Lys Asn His
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Leu Gln Thr His Asp Pro Asn Lys Met Ala Phe Gly Cys Glu Glu Cys
 85 90 95

Gly Lys Lys Tyr Asn Thr Met Leu Gly Tyr Lys Arg His Leu Ala Leu
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His Ala Ala Ser Ser Gly Asp Leu Thr Cys Gly Val Cys Ala Leu Glu
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Leu Gly Ser Thr Glu Val Leu Leu Asp His Leu Lys Ala His Ala Glu
 130 135 140

Glu Lys Pro Pro Ser Gly Thr Lys Glu Lys Lys His Gln Cys Asp His
 145 150 155 160

Cys Glu Arg Cys Phe Tyr Thr Arg Lys Asp Val Arg Arg His Leu Val
 165 170 175

Val His Thr Gly Cys Lys Asp Phe Leu Cys Gln Phe Cys Ala Gln Arg
 180 185 190

Phe Gly Arg Lys Asp His Leu Thr Arg His Thr Lys Lys Thr His Ser
 195 200 205

Gln Glu Leu Met Lys Glu Ser Leu Gln Thr Gly Asp Leu Leu Ser Thr
 210 215 220

Phe His Thr Ile Ser Pro Ser Phe Gln Leu Lys Ala Ala Ala Leu Pro
 225 230 235 240

Pro Phe Pro Leu Gly Ala Ser Ala Gln Asn Gly Leu Ala Ser Ser Leu
 245 250 255

Pro Ala Glu Val His Ser Leu Thr Leu Ser Pro Pro Glu Gln Ala Ala
 260 265 270

Gln Pro Met Gln Pro Leu Pro Glu Ser Leu Ala Ser Leu His Pro Ser
 275 280 285

Val Ser Pro Gly Ser Pro Pro Pro Pro Leu Pro Asn His Lys Tyr Asn
 290 295 300

Thr Thr Ser Thr Ser Tyr Ser Pro Leu Ala Ser Leu Pro Leu Lys Ala
 305 310 315 320

86

C

Asp Thr Lys Gly Phe Cys Asn Ile Ser Leu Phe Glu Asp Leu Pro Leu
 325 330 335
 Gln Glu Pro Gln Ser Pro Gln Lys Leu Asn Pro Gly Phe Asp Leu Ala
 340 345 350
 Lys Gly Asn Ala Gly Lys Val Asn Leu Pro Lys Glu Leu Pro Ala Asp
 355 360 365
 Ala Val Asn Leu Thr Ile Pro Ala Ser Leu Asp Leu Ser Pro Leu Leu
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 Gly Phe Trp Gln Leu Pro Pro Pro Ala Thr Gln Asn Thr Phe Gly Asn
 385 390 395 400
 Ser Thr Leu Ala Leu Gly Pro Gly Glu Ser Leu Pro His Arg Leu Ser
 405 410 415
 Cys Leu Gly Gln Gln Gln Gln Glu Pro Pro Leu Ala Met Gly Thr Val
 420 425 430
 Ser Leu Gly Gln Leu Pro Leu Pro Pro Ile Pro His Val Phe Ser Ala
 435 440 445
 Gly Thr Gly Ser Ala Ile Leu Pro His Phe His His Ala Phe Arg
 450 455 460